



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/689,677C

DATE: 07/22/2004

TIME: 09:43:46

Input Set : A:\08702.0093.ST25.txt

Output Set: N:\CRF4\07222004\J689677C.raw

3 <110> APPLICANT: Wolfman, Neil
 4 Bouxsein, Mary
 6 <120> TITLE OF INVENTION: ActRIIB Fusion Polypeptides and Uses Therefor
 8 <130> FILE REFERENCE: 08702.0093-00000
 10 <140> CURRENT APPLICATION NUMBER: US 10/689,677C
 11 <141> CURRENT FILING DATE: 2003-10-22
 13 <150> PRIOR APPLICATION NUMBER: US 60/421,041
 14 <151> PRIOR FILING DATE: 2002-10-25
 16 <160> NUMBER OF SEQ ID NOS: 6
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 512
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Human
 25 <400> SEQUENCE: 1

27 Met Thr Ala Pro Trp Val Ala Leu Ala Leu Trp Gly Ser Leu Cys
 28 1 5 10 15
 31 Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
 32 20 25 30
 35 Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
 36 35 40 45
 39 Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Ala
 40 50 55 60
 43 Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Gly Cys Trp Leu Asp
 44 65 70 75 80
 47 Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
 48 85 90 95
 51 Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
 52 100 105 110
 55 Phe Thr His Leu Pro Glu Ala Gly Pro Glu Val Thr Tyr Glu Pro
 56 115 120 125
 59 Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
 60 130 135 140
 63 Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
 64 145 150 155 160
 67 Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Asp Pro
 68 165 170 175
 71 Gly Pro Pro Pro Ser Pro Leu Val Gly Leu Lys Pro Leu Gln Leu
 72 180 185 190
 75 Leu Glu Ile Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala Gln
 76 195 200 205
 79 Leu Met Asn Asp Phe Val Ala Val Lys Ile Phe Pro Leu Gln Asp Lys
 80 210 215 220



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83 Gln Ser Trp Gln Ser Glu Arg Glu Ile Phe Ser Thr Pro Gly Met Lys
 84 225 230 235 240
 87 His Glu Asn Leu Leu Gln Phe Ile Ala Ala Glu Lys Arg Gly Ser Asn
 88 245 250 255
 91 Leu Glu Val Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly Ser
 92 260 265 270
 95 Leu Thr Asp Tyr Leu Lys Gly Asn Ile Ile Thr Trp Asn Glu Leu Cys
 96 275 280 285
 99 His Val Ala Glu Thr Met Ser Arg Gly Leu Ser Tyr Leu His Glu Asp
 100 290 295 300
 103 Val Pro Trp Cys Arg Gly Glu Gly His Lys Pro Ser Ile Ala His Arg
 104 305 310 315 320
 107 Asp Phe Lys Ser Lys Asn Val Leu Leu Lys Ser Asp Leu Thr Ala Val
 108 325 330 335
 111 Leu Ala Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro Pro
 112 340 345 350
 115 Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro Glu
 116 355 360 365
 119 Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg Ile
 120 370 375 380
 123 Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Val Ser Arg Cys
 124 385 390 395 400
 127 Lys Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu Glu
 128 405 410 415
 131 Glu Ile Gly Gln His Pro Ser Leu Glu Glu Leu Gln Glu Val Val Val
 132 420 425 430
 135 His Lys Met Arg Pro Thr Ile Lys Asp His Trp Leu Lys His Pro
 136 435 440 445
 139 Gly Leu Ala Gln Leu Cys Val Thr Ile Glu Glu Cys Trp Asp His Asp
 140 450 455 460
 143 Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Glu Glu Arg Val Ser Leu
 144 465 470 475 480
 147 Ile Arg Arg Ser Val Asn Gly Thr Thr Ser Asp Cys Leu Val Ser Leu
 148 485 490 495
 151 Val Thr Ser Val Thr Asn Val Asp Leu Pro Pro Lys Glu Ser Ser Ile
 152 500 505 510
 155 <210> SEQ ID NO: 2
 156 <211> LENGTH: 375
 157 <212> TYPE: PRT
 158 <213> ORGANISM: Human
 160 <400> SEQUENCE: 2
 162 Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile
 163 1 5 10 15
 166 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 167 20 25 30
 170 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 171 35 40 45
 174 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 175 50 55 60

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178 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
 179 65 70 75 80
 182 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 183 85 90 95
 186 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 187 100 105 110
 190 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
 191 115 120 125
 194 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 195 130 135 140
 198 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 199 145 150 155 160
 202 Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 203 165 170 175
 206 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 207 180 185 190
 210 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 211 195 200 205
 214 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 215 210 215 220
 218 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 219 225 230 235 240
 222 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
 223 245 250 255
 226 Val Thr Asp Thr Pro Lys Arg Ser Arg Asp Phe Gly Leu Asp Cys
 227 260 265 270
 230 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 231 275 280 285
 234 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 235 290 295 300
 238 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 239 305 310 315 320
 242 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 243 325 330 335
 246 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 247 340 345 350
 250 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 251 355 360 365
 254 Val Asp Arg Cys Gly Cys Ser
 255 370 375
 258 <210> SEQ ID NO: 3
 259 <211> LENGTH: 378
 260 <212> TYPE: PRT
 261 <213> ORGANISM: Artificial Sequence
 263 <220> FEATURE:
 264 <223> OTHER INFORMATION: Chimera/Fusion
 266 <400> SEQUENCE: 3
 268 Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
 269 1 5 10 15

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272 Ser Tyr Ile Tyr Ala Thr Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu
 273 20 25 30
 276 Cys Ile Tyr Tyr Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser
 277 35 40 45
 280 Gly Leu Glu Arg Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr
 281 50 55 60
 284 Ala Ser Trp Arg Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly
 285 65 70 75 80
 288 Cys Trp Leu Asp Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala
 289 85 90 95
 292 Thr Glu Glu Asn Pro Gln Val Tyr Phe Cys Cys Glu Gly Asn Phe
 293 100 105 110
 296 Cys Asn Glu Arg Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val
 297 115 120 125
 300 Thr Tyr Glu Pro Pro Pro Thr Ala Pro Thr Gly Gly Arg Gly Asp Asp
 301 130 135 140
 304 Asp Asp Lys Thr Arg Ser Arg Asp Lys Thr His Thr Cys Pro Pro Cys
 305 145 150 155 160
 308 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 309 165 170 175
 312 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 313 180 185 190
 316 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 317 195 200 205
 320 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 321 210 215 220
 324 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 325 225 230 235 240
 328 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 329 245 250 255
 332 Lys Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 333 260 265 270
 336 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 337 275 280 285
 340 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 341 290 295 300
 344 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 345 305 310 315 320
 348 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 349 325 330 335
 352 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 353 340 345 350
 356 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 357 355 360 365
 360 Gln Lys Ser Leu Ser Leu Ser Pro Pro Lys
 361 370 375
 364 <210> SEQ ID NO: 4
 365 <211> LENGTH: 1134
 366 <212> TYPE: DNA

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367 <213> ORGANISM: Artificial Sequence
369 <220> FEATURE:
370 <223> OTHER INFORMATION: Chimera/Fusion
372 <400> SEQUENCE: 4

373	atgaaaattct	tagtcaacgt	tgccttgtt	tttatggtcg	tgtacatttc	ttacatctat	60
375	gcgactagtg	ggcgtggga	ggctgagaca	cgggagtgca	tctactacaa	cgcactgg	120
377	gagctggagc	gcaccaacca	gagcggcctg	gagcgtcg	aaggcgagca	ggacaagcgg	180
379	ctgcactgct	acgcctcctg	gjcacacgc	tctggcacca	tgcagctcg	gaagaaggc	240
381	tgcggctag	atgactcaa	ctgtacgat	aggcaggagt	gtgtggccac	tgaggagaac	300
383	ccccagggt	acttctgctg	ctgtgaaggc	aacttctgca	acgagcgctt	cactcattg	360
385	ccagaggctg	ggggcccgga	agtacacgtac	gagccacccc	cgacagcccc	caccggcggc	420
387	cgcggagacg	acgacgacaa	gacgcgttct	agagacaaaa	ctcacacatg	cccacccgtgc	480
389	ccagcacctg	aactcctggg	ggaccgtca	gtcttcctct	tccccccaaa	acccaaggac	540
391	accctcatga	tctccggac	ccctgaggtc	acatgcgtgg	tgttgacgt	gagccacgaa	600
393	gaccctgagg	tcaagttcaa	ctggtaacgtg	gacggcgtgg	aggtgcataa	tgccaagaca	660
395	aagccgcggg	aggagcagta	caacagcag	taccgtgtgg	tcaagcgtcct	caccgtcctg	720
397	caccaggact	ggctaatgg	caaggagttac	aagtgcagg	tctccaacaa	agccctccca	780
399	gtccccatcg	agaaaaaccat	ctccaaagcc	aaagggcagc	cccgagaacc	acaggtgtac	840
401	accctgcctcc	catcccgga	ggagatgacc	aagaaccagg	tcagcctgac	ctgcctggc	900
403	aaaggcttct	atcccagcga	catcgccgtg	gagtggaga	gcaatggca	gccggagaac	960
405	aactacaaga	ccacgcctcc	cgtgctggac	tccgacggct	cottcttcct	ctatagcaag	1020
407	ctcaccgtgg	acaagagcag	gtggcagcag	gggaacgtct	tctcatgctc	cgtgatgcat	1080
409	gaggctctgc	acaaccacta	cacgcagaag	agcctctccc	tgtccccgcc	taaa	1134

412 <210> SEQ ID NO: 5

413 <211> LENGTH: 4

414 <212> TYPE: PRT

415 <213> ORGANISM: Artificial Sequence

417 <220> FEATURE:

418 <223> OTHER INFORMATION: Linking Sequence, Gly-Ser repeat

420 <400> SEQUENCE: 5

422 Gly Ser Gly Ser

423 1

426 <210> SEQ ID NO: 6

427 <211> LENGTH: 4

428 <212> TYPE: PRT

429 <213> ORGANISM: Artificial Sequence

431 <220> FEATURE:

432 <223> OTHER INFORMATION: Linking Sequence, Enterokinase Cleavage Site

434 <400> SEQUENCE: 6

436 Asp Asp Asp Lys

437 1

VERIFICATION SUMMARY

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